

i5k Insect and other Arthropod Genome Sequencing Initiative



<http://arthropodgenomes.org/wiki/i5K>

aims:

- sequence 5000 insect/arthropod genomes in 5 years
- form international community for support & advice

to include:

- *all species* important to worldwide agriculture, food safety, medicine, energy production, etc.
- *every branch* of arthropod phylogeny
- *major* models in biology
- *most abundant* worldwide

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membership:

- broad and inclusive – scientists around the world
- self-selected (*join on the i5k wiki*)

funding:

- academia, government, industry, private sources
- collaborative or individual

species:

- *nominate on the i5k wiki!*

i5k Working groups ~ pls join!

- ❖ Funding and resources (Owain Edwards)
- ❖ 2012 workshop and training (Jay Evans)
- ❖ Criteria for arthropod prioritization (Michael Pfrender)
- ❖ Phylogenomics/Evolutionary Genomics (Toni Gabaldon)
- ❖ Community access/website (Daniel Lawson)
- ❖ Post sequencing bioinformatics Daniel Lawson (interim)
- ❖ Community curation (Alexie Papanicolaou, Monica Munoz-Torres)
- ❖ Outreach (Marian Goldsmith)



Nominations 08-13:

807 species

702 Hexapoda

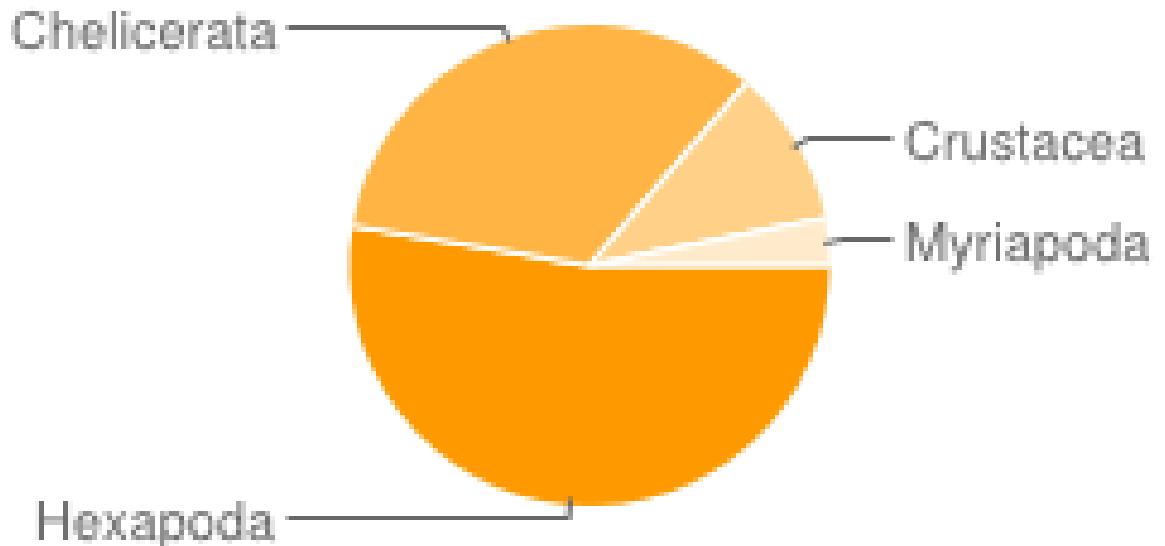
64 Chelicerata

20 Crustacea

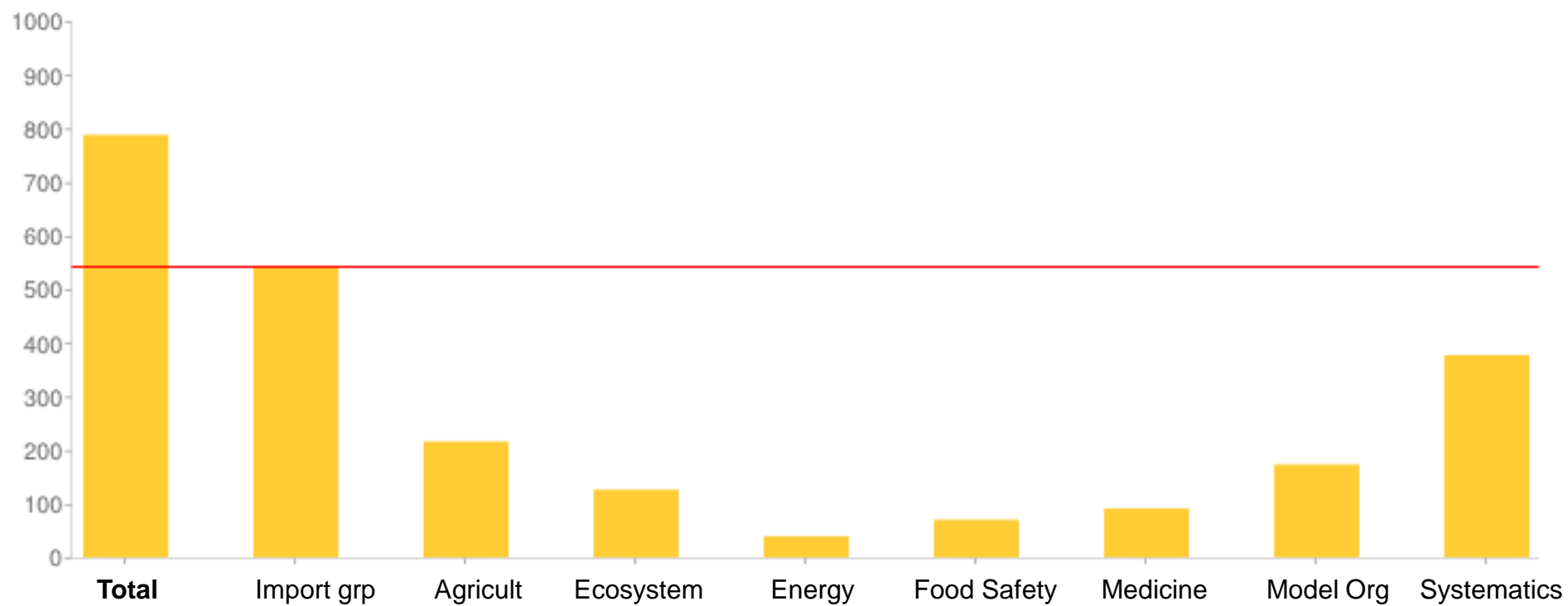
6 Myriapoda



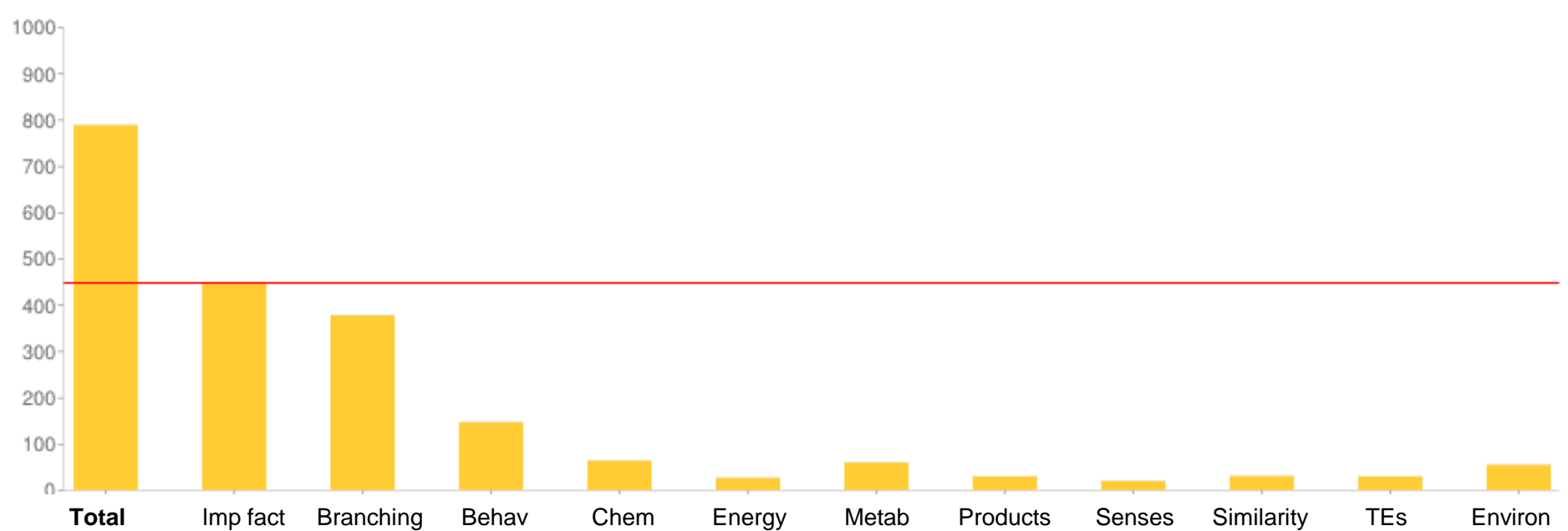
Species by Subphylum



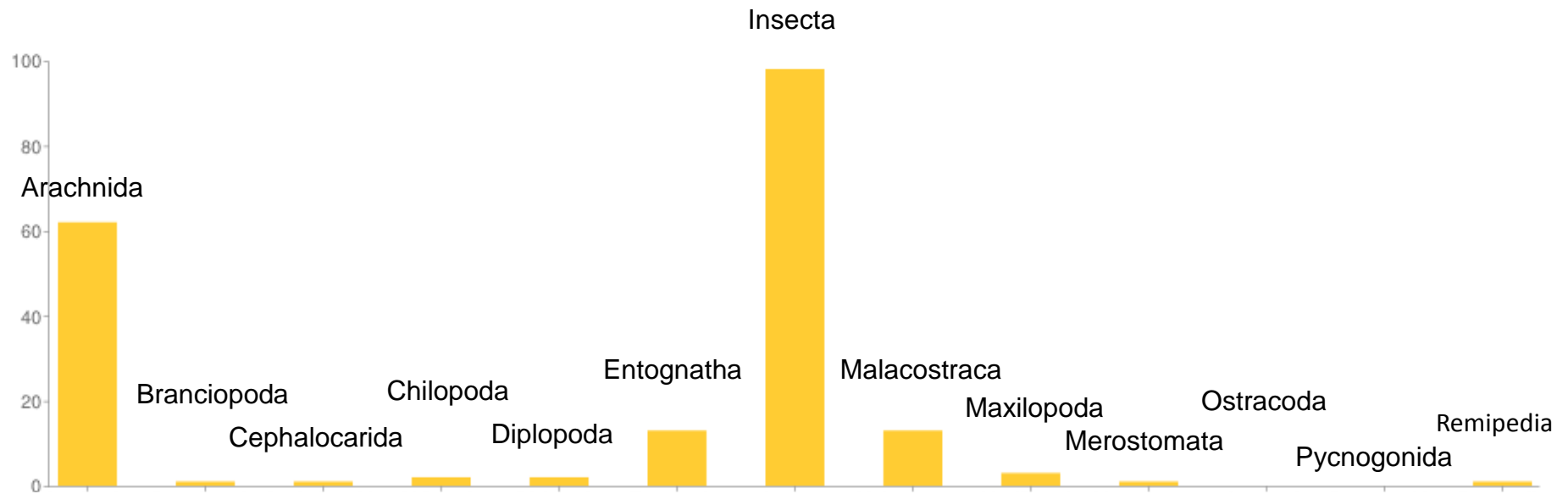
Importance groups



Impact factors for i5k nominations



Nominations by Class



50 spp: Baylor College of Medicine Human Genome Sequencing Center



<http://www.hgsc.bcm.tmc.edu/content/i5k-project>



Selection criteria

Biological Relevance and Societal Impact

Agriculture, human health, evolution, ecology, biodiversity, conservation
Model system potential (community size, interdisciplinary)
Phylogenetic placement (representative or comparative studies; overlap)
Metagenomic discovery (assoc'ns with parasites, parasitoids, or symbionts)

Feasibility: Available resources

Genomic (genetic maps, ESTs, recombinant inbred lines)
Availability/development of cultured /inbred strains
Genome size (1 large vs several small)
Enough material (DNA/RNA)
Community support (annotation, end usage, database mgt)

Identified project leader(s)

Justifies selection criteria (white paper)
Delivers DNA/RNA to the Genome Center
Coordinates community analysis and publication

33 Genome Sequences now in progress for



Order	No specimens
Amphipod	1
Arachnida	3
Archaeognatha	1
Coleoptera	4
Collembola	1
Copepod	1
Dictyoptera	1
Diplura	1
Diptera	2
Ephemeraidae	1
Hemiptera	6
Hymenoptera	4
Neuroptera	1
Odonata	1
Onychophora	1
Protura	1
Scorpiones	1
Thysanoptera	1
Trichoptera	1
Total	33

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Lepidopteran genome projects

~ *in progress*, *funded*, ***finished***, or *nearly so*

Moths

Bombyx mori (Mita, NIAS; Xia, SWU) – **publ. Dec. 2004**

Bombyx mandarina (Xia, SWU; BGI)

Manduca sexta (Kanost, Blissard et al., KSU; Baylor)

Helicoverpa armigera, *H. assulta*, *H. zea*

(Gordon et al., CSIRO; Baylor)

Heliothis virescens, *H. subflexa* (Hopper, USDA)

Spodoptera frugiperda (Fournier et al., Montpellier;

Genoscope); *Spodoptera litura* (Mita, Xia, SWU)

Plutella xylostella (Fujian University, BGI) – **publ. Jan. 2013**

Amyelois transitella (Robertson, Berenbaum, U. Ill.)

Lymantria dispar (Gunderson-Rindal, USDA)

Biston betularia (Saccheri, Liverpool)

Epiphyas postvittana, *Ctenopseustis obliquana*, *Planotortrix octo*

(Newcomb, Plant & Food Res. NZ)



Lepidopteran genome projects

Butterflies

Danaus plexippus (Reppert, U. Mass. Med.; Boore,
Genome Project Solns) – published Nov. 2011



Heliconius melpomene, *H. erato*, *H. numata* (Jiggins,
Mallet, McMillan, et al., Cambridge, STRI; Baylor)
–published July 2012



Melitaea cinxia (Hanski, U. Helsinki)



Papilio xuthus, *P. polytes* (Fujiwara, U. Tokyo); *P. xuthus*,
P. machaon, *P. protenor* (BGI)

Pararge aegeria (Breuker, Gibbs, Oxford)

Bicyclus anynana (Brakefield, Blaxter, Cambridge,
Edinburgh)



Other info on molecular biology, genetics and genomics of Lepidoptera

- ❖ Lepgen-L listserv (ask MG to join)
- ❖ International Workshop on Molecular Biology and Genetics of Lepidoptera – Kolymbari, Crete
3 yr intervals; next one August 2014?
- ❖ Genome databases – KaikoBase, SilkDB, Butterflygenome, Monarchbase, Konagabase, Agripestbase, Spodobase, etc.